

CLAIM AMENDMENTS

1-31. (canceled)

32. (currently amended): A method of detecting ~~post-transcriptional~~ gene silencing (PTGS) of a target gene in an organism which method comprises the steps of:

detecting in a nucleic acid extract prepared from said organism ~~in which organism it is suspected that PTGS is occurring to determine~~ the presence as opposed to the absence of short RNA molecules (SRMs) of uniform length which are 20-30 nucleotides in length in said extract,

characterizing any SRMs which are present in said extract wherein said characterizing comprises determining identity or similarity with said target gene,

wherein the presence of any SRMs having identity or similarity with said target gene indicates silencing of said target gene in the organism, and

confirming that said target gene has been silenced;

wherein said organism is selected from the group consisting of plants, insects, mammals, fish, reptiles and birds.

33. (withdrawn): The method of claim 32, wherein the organism is a plant.

34. (withdrawn): The method of claim 32, wherein the organism is an insect or a mammal or a bird.

35. (previously presented): The method of claim 32, wherein the organism is a mammal.

36. (previously presented): The method of claim 32 wherein the SRMs are short antisense RNA molecules (SARMs).

37. (previously presented): The method of claim 32 wherein the SRMs are short sense RNA molecules (SSRMs).

38-40. (canceled)

41. (previously presented): The method of claim 32, wherein the step of characterizing any SRMs present in the extract to determine identity or similarity with a target gene is performed by a process that comprises:

tagging said SRMs with a marker, and
probing a library of genes from said organism, and
identifying the genes in said library that bind to said SRMs whereby a gene that binds to said SRM is identified as said target gene which is silenced.

42-48. (canceled)

49. (previously presented): The method of claim 32, wherein said short RNA molecules are 20-25 nucleotides in length.

50-65. (canceled)

66. (previously presented): The method of claim 32 wherein said determining identity or similarity comprises determining sequence identity or similarity.

67. (previously presented): The method of claim 32 wherein the SRMs comprise both short antisense RNA molecules (SARMs) and short sense RNA molecules (SSRMs).

68. (new): The method of claim 32 wherein said characterizing comprises determining identity with the target gene.

69. (new): The method of claim 68 wherein said determining identity comprises determining sequence identity.

70. (new): The method of claim 32 wherein, as a result of said characterizing, sequences of SRMs effective in inducing silencing of said target gene in said organism are determined.

71. (new): The method of claim 32 wherein said SRMs are 20 nucleotides in length.

72. (new): The method of claim 32 wherein said SRMs are 21 nucleotides in length.
73. (new): The method of claim 32 wherein said SRMs are 22 nucleotides in length.
74. (new): The method of claim 32 wherein said SRMs are 23 nucleotides in length.
75. (new): The method of claim 32 wherein said SRMs are 24 nucleotides in length.
76. (new): The method of claim 32 wherein said SRMs are 25 nucleotides in length.
77. (new): The method of claim 32 wherein said SRMs are 26 nucleotides in length.
78. (new): The method of claim 32 wherein said SRMs are 27 nucleotides in length.
79. (new): The method of claim 32 wherein said SRMs are 28 nucleotides in length.
80. (new): The method of claim 32 wherein said SRMs are 29 nucleotides in length.
81. (new): The method of claim 32 wherein said SRMs are 30 nucleotides in length.
82. (new): A method of detecting gene silencing of a target gene in an organism which method comprises the steps of:
- detecting in a nucleic acid extract prepared from said organism the presence as opposed to the absence of short RNA molecules (SRMs) of uniform length which are 20-30 nucleotides in length in said extract,
- characterizing any SRMs which are present in said extract wherein said characterizing comprises determining identity with said target gene,
- wherein the presence of any SRMs having identity with said target gene indicates silencing of said target gene in the organism,
- wherein said organism is selected from the group consisting of plants, insects, mammals, fish, reptiles and birds.

83. (new): The method of claim 82, which further includes confirming that said target gene has been silenced.